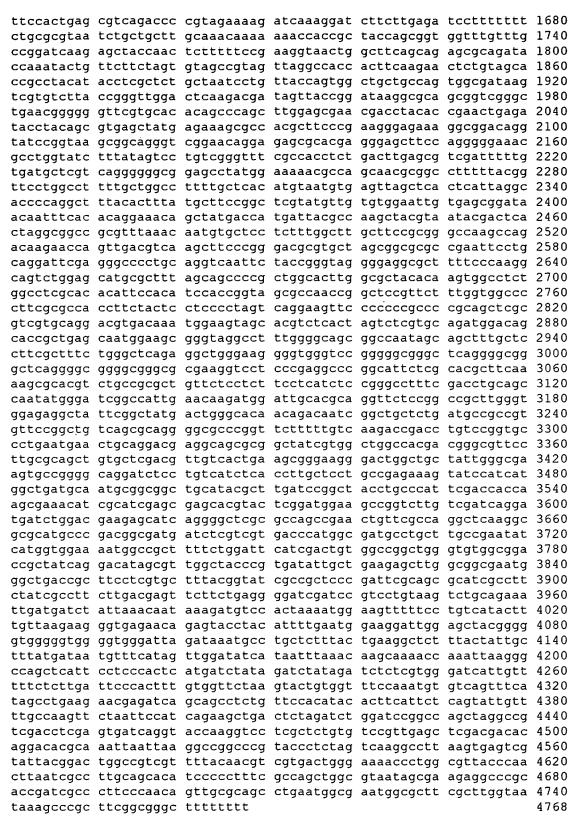
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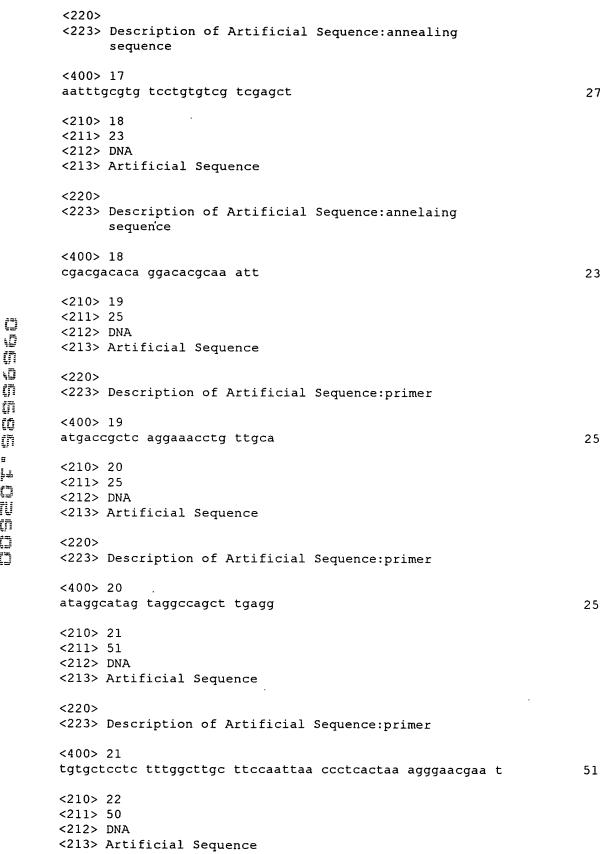
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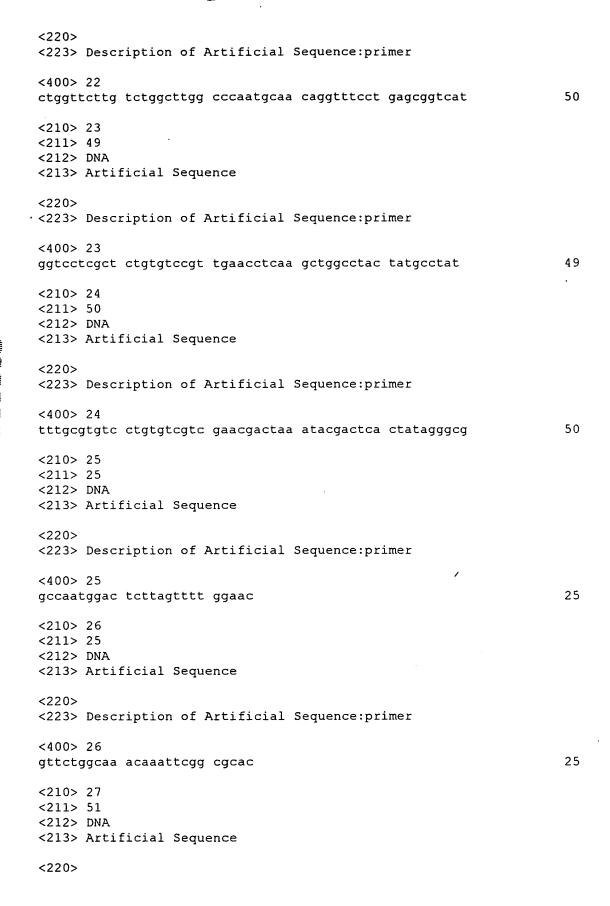
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<211> 471
<212> DNA
<213> homologue of T243
<220>
<221> modified base
<222> (260)
<223> A, T, G or C
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cgagcgaacc cattggttgn gtcgcccgcg ggccttggtc ggtttcgcaa gccgctagag 300
qctaccqqqc qaqqqqcqqq ccqqaqctcq ccqttqccqt qqttacccaq aqacacqtqc 360
qcaqtcccqq aagcggccgg gggaagctgc tccqcqcqcq ctqccqqaqq aagcqccqcc 420
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<211> 370
<212> DNA
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ctggagatcc ctgcttttgg gcgaatccgg gggtagttgc tcatcaagac tagaggtggg 240
ggtggaggga aggcttcata caggaagcct gctgcgaaat gaagagttgg ccagggaaag 300
catggcgtgc agaggaactc actccgcaga aaccacagaa acagaggcag atgaggacgc 360
cctgccggcc
<210> 52
<211> 276
<212> PRT
<213> murine TRP
<400> 52
Met Glu Ser Met Ser Glu Leu Ala Pro Arg Cys Leu Leu Phe Pro Leu
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Leu Leu Leu Pro Leu Leu Leu Pro Ala Pro Lys Leu Gly Pro
                                25
Ser Pro Ala Gly Ala Glu Glu Thr Asp Trp Val Arg Leu Pro Ser Lys
        35
                            40
Cys Glu Val Cys Lys Tyr Val Ala Val Glu Leu Lys Ser Ala Phe Glu
Glu Thr Gly Lys Thr Lys Glu Val Ile Asp Thr Gly Tyr Gly Ile Leu
65
                    70
Asp Gly Lys Gly Ser Gly Val Lys Tyr Thr Lys Ser Asp Leu Arg Leu
Ile Glu Val Thr Glu Thr Ile Cys Lys Arg Leu Leu Asp Tyr Ser Leu
           100
                               105
His Lys Glu Arg Thr Gly Ser Asn Arg Phe Ala Lys Gly Met Ser Glu
       115
                           120
                                              125
Thr Phe Glu Thr Leu His Asn Leu Val His Lys Gly Val Lys Val Val
    130
                       135
                                          140
```



```
Met Asp Ile Pro Tyr Glu Leu Trp Asn Glu Thr Ser Ala Glu Val Ala
Asp Leu Lys Lys Gln Cys Asp Val Leu Val Glu Glu Phe Glu Glu Val
                                    170
                165
                                                        175
Ile Glu Asp Trp Tyr Arg Asn His Gln Glu Glu Asp Leu Thr Glu Phe
                                185
Leu Cys Ala Asn His Val Leu Lys Gly Lys Asp Thr Ser Cys Leu Ala
                            200
                                                205
Glu Arg Trp Ser Gly Lys Lys Gly Asp Ile Ala Ser Leu Gly Gly Lys
Lys Ser Lys Lys Arg Ser Gly Val Lys Gly Ser Ser Ser Gly Ser
                                        235
Ser Lys Gln Arg Lys Glu Leu Gly Gly Leu Gly Glu Asp Ala Asn Ala
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                                    250
Glu Glu Glu Gly Val Gln Lys Ala Ser Pro Leu Pro His Ser Pro
            260
                                265
Pro Asp Glu Leu
       275
<210> 53
<211> 1848
<212> DNA
<213> expanded T243
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ctgctgctgc tgctgctgct gctgctgctg ctgctgctgc tgctgctgct gctgctgctg 180
ctgctgctgc tgcgattgcc cagcaaatgc gaagtgtgca agtatgttgc tgtggagctg 240
aagtoggott ttgaggaaac gggaaagaco aaggaagtga ttgacaccgg ctatggcatc 300
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actgagacca tttgcaagag gcttctggac tacagcctgc acaaggagag gactggcagc 420
aaccggtttg ccaagggtat gtcggagacc tttgagacgc tgcacaacct agtccacaa 480
ggggtcaagg tggtgatgga tatcccctat gagctgtgga acgagacctc agcagaggtg 540
gctgacctca agaagcagtg tgacgtgctg gtggaagagt ttgaagaggt gattgaggac 600
tggtacagga accaccagga ggaagacctg actgaattcc tctgtgccaa ccacgtgctg 660
aagggaaagg acacgagttg cctagcagag cggtggtctg gcaagaaggg ggacatagcc 720
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agcagcaagc agaggaagga actggggggc ctgggggagg atgccaacgc cgaggaggag 840
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cttagtgtcc ttgaatcaag accectgact teagagettg ggacaegeae agegeagege 960
agegeagete cageaaggae agetgetgte cageateagg tetecteest tggetgtgee 1020
cctttccttc ccttgaacaa cagcaagagg tggaaggatc tggggtgctg ggagacggca 1080
ccccaaaggg aagaggagga ggagcagaag gcagctctct ttctacacag tccccctcac 1140
gageteeggg gtecacecag cateeecagg etgagateea ggeteetgae atggaagetg 1200
aaqaqcatga qqcacataaq atqctcacca qcqccccctt caqccaqqaa qqactccqtq 1260
```

cagceteage agecaggeet geetetteet tecaceaage attetettet getggteett 1320



```
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<400> 54

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Gly Ile Leu Asp Gly Lys Gly Ser Gly Val Lys Tyr Thr Lys Ser Asp 85 90 95

Leu Arg Leu Ile Glu Val Thr Glu Thr Ile Cys Lys Arg Leu Leu Asp 100 105 110

Tyr Ser Leu His Lys Glu Arg Thr Gly Ser Asn Arg Phe Ala Lys Gly
115 120 125

Met Ser Glu Thr Phe Glu Thr Leu His Asn Leu Val His Lys Gly Val 130 135 140

Lys Val Val Met Asp Ile Pro Tyr Glu Leu Trp Asn Glu Thr Ser Ala 145 150 155 160

Glu Val Ala Asp Leu Lys Lys Gln Cys Asp Val Leu Val Glu Glu Phe
165 170 175

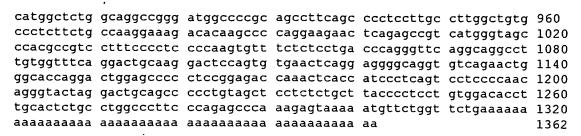
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Thr Glu Phe Leu Cys Ala Asn His Val Leu Lys Gly Lys Asp Thr Ser 195 200 205

Cys Leu Ala Glu Arg Trp Ser Gly Lys Lys Gly Asp Ile Ala Ser Leu 210 215 220



```
Gly Gly Lys Lys Ser Lys Lys Lys Arg Ser Gly Val Lys Gly Ser Ser
Ser Gly Ser Ser Lys Gln Arg Lys Glu Leu Gly Gly Leu Gly Glu Asp
                245
                                    250
Ala Asn Ala Glu Glu Glu Gly Val Gln Lys Ala Ser Pro Leu Pro
                                265
His Ser Pro Pro Asp Glu Leu
        275
<210> 55
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
<400> 55
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                                                                   25
<210> 56
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
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acttcgcatt tgctgggcaa tcgca
                                                                  25
<210> 57
<211> 1362
<212> DNA
<213> human TRP
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gagaacgact gggttcgcct gcccagcaaa tgcgaagtgt gtaaatatgt tgctgtggag 180
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gactggtaca ggaaccacca ggaggaagac ctgactgaat tcctctgcgc caaccacgtg 600
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<210> 58

<211> 278

<212> PRT

<213> human TRP

<400> 58

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20 25 30

Ser Gln Ala Gly Ala Glu Glu Asn Asp Trp Val Arg Leu Pro Ser Lys 35 40 45

Cys Glu Val Cys Lys Tyr Val Ala Val Glu Leu Lys Ser Ala Phe Glu 50 55 60

Glu Thr Gly Lys Thr Lys Glu Val Ile Gly Thr Gly Tyr Gly Ile Leu 65 70 75 80

Asp Gln Lys Ala Ser Gly Val Lys Tyr Thr Lys Ser Asp Leu Arg Leu 85 90 95

Ile Glu Val Thr Glu Thr Ile Cys Lys Arg Leu Leu Asp Tyr Ser Leu 100 105 110

His Lys Glu Arg Thr Gly Ser Asn Arg Phe Ala Lys Gly Met Ser Glu 115 120 125

Thr Phe Glu Thr Leu His Asn Leu Val His Lys Gly Val Lys Val Val 130 135 140

Met Asp Ile Pro Tyr Glu Leu Trp Asn Glu Thr Ser Ala Glu Val Ala 145 150 155 160

Asp Leu Lys Lys Gln Cys Asp Val Leu Val Glu Glu Phe Glu Glu Val 165 170 175

Ile Glu Asp Trp Tyr Arg Asn His Gln Glu Glu Asp Leu Thr Glu Phe
180 185 190

Leu Cys Ala Asn His Val Leu Lys Gly Lys Asp Thr Ser Cys Leu Ala 195 200 205

Glu Gln Trp Ser Gly Lys Lys Gly Asp Thr Ala Ala Leu Gly Gly Lys 210 215 220





Lys Ser Lys Lys Lys Ser Ser Arg Ala Lys Ala Ala Gly Gly Arg Ser 225 230 235 240

Ser Ser Ser Lys Gln Arg Lys Glu Leu Gly Gly Leu Glu Gly Asp Pro 245 250 255

Ser Pro Glu Glu Asp Glu Gly Ile Gln Lys Ala Ser Pro Leu Thr His 260 265 270

Ser Pro Pro Asp Glu Leu 275

<210> 59

<211> 107

<212> DNA

<213> deletion generated by knockout

<400> 59